Yanay Ofran

List of Publications by Year
in descending order

39 papers	3,218 citations	257450 24 h-index	345221 36 g-index
39 all docs	39 docs citations	39 times ranked	4268 citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting the actin nucleation promoting factor WASp provides a therapeutic approach for hematopoietic malignancies. Nature Communications, 2021, 12, 5581.	12.8	8
2	Integrating genomic data from high-throughput studies with computational modeling reveals differences in the molecular basis of hyposalivation between type 1 and type 2 diabetes. Clinical Oral Investigations, 2018, 22, 151-159.	3.0	2
3	Antibody Modeling, Engineering, and Design. , 2018, , 1-8.		0
4	Computational Design of Epitope-Specific Functional Antibodies. Cell Reports, 2018, 25, 2121-2131.e5.	6.4	55
5	Computational design of antibodies. Current Opinion in Structural Biology, 2018, 51, 156-162.	5.7	48
6	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	2.5	39
7	De-novo protein function prediction using DNA binding and RNA binding proteins as a test case. Nature Communications, 2016, 7, 13424.	12.8	22
8	How far from the SNP may the causative genes be?. Nucleic Acids Research, 2016, 44, 6046-6054.	14.5	138
9	Understanding differences between synthetic and natural antibodies can help improve antibody engineering. MAbs, 2016, 8, 278-287.	5.2	18
10	Antibody specific epitope prediction—emergence of a new paradigm. Current Opinion in Virology, 2015, 11, 98-102.	5.4	64
11	PEASE: predicting B-cell epitopes utilizing antibody sequence. Bioinformatics, 2015, 31, 1313-1315.	4.1	51
12	Large Scale Analysis of Phenotype-Pathway Relationships Based on GWAS Results. PLoS ONE, 2014, 9, e100887.	2.5	14
13	Potent Neutralization of Vaccinia Virus by Divergent Murine Antibodies Targeting a Common Site of Vulnerability in L1 Protein. Journal of Virology, 2014, 88, 11339-11355.	3.4	40
14	Large‐scale analysis of somatic hypermutations in antibodies reveals which structural regions, positions and amino acids are modified to improve affinity. FEBS Journal, 2014, 281, 306-319.	4.7	45
15	Using a Combined Computational-Experimental Approach to Predict Antibody-Specific B Cell Epitopes. Structure, 2014, 22, 646-657.	3.3	63
16	Co-expression and co-localization of hub proteins and their partners are encoded in protein sequence. Molecular BioSystems, 2014, 10, 787.	2.9	1
17	Computational Identification of Antigen-Binding Antibody Fragments. Journal of Immunology, 2013, 190, 2327-2334.	0.8	21
18	The indistinguishability of epitopes from protein surface is explained by the distinct binding preferences of each of the six antigen-binding loops. Protein Engineering, Design and Selection, 2013, 26, 599-609.	2.1	82

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19	The Structural Basis of Antibody-Antigen Recognition. Frontiers in Immunology, 2013, 4, 302.	4.8	361
20	A Systematic Comparison of Free and Bound Antibodies Reveals Binding-Related Conformational Changes. Journal of Immunology, 2012, 189, 4890-4899.	0.8	96
21	Paratome: an online tool for systematic identification of antigen-binding regions in antibodies based on sequence or structure. Nucleic Acids Research, 2012, 40, W521-W524.	14.5	126
22	Structural Consensus among Antibodies Defines the Antigen Binding Site. PLoS Computational Biology, 2012, 8, e1002388.	3.2	99
23	Unveiling Protein Functions through the Dynamics of the Interaction Network. PLoS ONE, 2011, 6, e17679.	2.5	14
24	Lateral acquisition of genes is affected by the friendliness of their products. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 343-348.	7.1	21
25	The Two Cultures and Systems Biology: How Philosophy Starts Where Science Ends. European Legacy, 2008, 13, 589-604.	0.2	2
26	Automated Identification of Complementarity Determining Regions (CDRs) Reveals Peculiar Characteristics of CDRs and B Cell Epitopes. Journal of Immunology, 2008, 181, 6230-6235.	0.8	73
27	MOLECULAR BIOINFORMATICS FOR DISEASE â€" SESSION INTRODUCTION. , 2008, , .		0
28	The Rough Guide to In Silico Function Prediction, or How To Use Sequence and Structure Information To Predict Protein Function. PLoS Computational Biology, 2008, 4, e1000160.	3.2	83
29	Proteinâ€"Protein Interaction Hotspots Carved into Sequences. PLoS Computational Biology, 2007, 3, e119.	3.2	229
30	Prediction of DNA-binding residues from sequence. Bioinformatics, 2007, 23, i347-i353.	4.1	157
31	ISIS: interaction sites identified from sequence. Bioinformatics, 2007, 23, e13-e16.	4.1	243
32	Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. Journal of Molecular Recognition, 2007, 20, 75-82.	2.1	209
33	MOLECULAR BIOINFORMATICS FOR DISEASE: PROTEIN INTERACTIONS AND PHENOMICS â€" Session Introduction. , 2007, , .		0
34	Epitome: database of structure-inferred antigenic epitopes. Nucleic Acids Research, 2006, 34, D777-D780.	14.5	78
35	Proteins of the same fold and unrelated sequences have similar amino acid composition. Proteins: Structure, Function and Bioinformatics, 2006, 64, 275-279.	2.6	26
36	Create and assess protein networks through molecular characteristics of individual proteins. Bioinformatics, 2006, 22, e402-e407.	4.1	6

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37	Beyond annotation transfer by homology: novel protein-function prediction methods to assist drug discovery. Drug Discovery Today, 2005, 10, 1475-1482.	6.4	84
38	Analysing Six Types of Protein–Protein Interfaces. Journal of Molecular Biology, 2003, 325, 377-387.	4.2	378
39	Predicted protein-protein interaction sites from local sequence information. FEBS Letters, 2003, 544, 236-239.	2.8	222